APPENDIX B: CLEAN COPY OF PENDING CLAIMS (UNOFFICIAL)

1. A method for identifying a subject at risk for the development of lung cancer comprising:

(a) obtaining a test sample from a subject;
(b) providing an RPL14, CD39L3, PMGM, or GC20 gene probe;
(c) contacting said probe with said test sample; and
(d) analyzing DNA from said test sample for loss of heterozygosity in RPL14,

whereby aberrations in the hybridization of said probe to said DNA loss of RPL14 heterozyosity, as compared to wild-type DNA, indicates risk for the development of lung cancer.

2. The method of claim 1, wherein said test sample comprises a surgical or biopsy specimen, a paraffin embedded tissue, a frozen tissue imprint, a sputum, a lavages, a peripheral blood lymphocytes, a urinary specimen such as a bladder washing and urine, esophageal brush, a fine needle aspiration, a buccal smear or a bronchial lavage.

3. The method of claim 1, wherein said cancer is lung cancer further comprising providing a GC20 gene probe and performing steps (c) and (d) with said GC20 gene probe.

4. The method of claim 1, wherein said cancer is an upper airway primary or secondary cancer.

11. The method of claim 1, wherein said subject is a smoker.

12. The method of claim 1, wherein said subject is a former smoker.

13. The method of claim 1, wherein said subject is a non-smoker.

14. The method of claim 1, wherein said test sample comes from said subject who has not previously been diagnosed with cancer.

15. The method of claim 1, wherein said probe is labeled with a fluorophore.

16. The method of claim 1, wherein said probe is labeled with digoxigenin.

17. The method of claim 1, wherein said probe size is between 1000 and 2000 base pairs.

18. The method in claim 1, further comprising a spiral CT-scan.

19. The method of claim 1, further comprising administering to said subject chemopreventive drugs, nutritional supplements, chemotherapeutic drugs or biological modifying [respdase] response drugs.

20. The method of claim 1, wherein said method is used to identify subjects who need an intensive follow-up protocol.

21. The probe method of claim 1, wherein said probe is used to identify subjects who are suitable for novel investigational therapeutic approaches.

22. The method of claim 1, wherein a control probe is used.

23. The method of claim 22, wherein said control probe is labeled with a fluorophore.

24. The method of claim 23, wherein said control probe is labeled with spectrum orange.

25. The method of claim 22, wherein said control probe is a chromosome 3 stable marker.

26. The method of claim 25, wherein said control probe is Centromere 3 (CEP 3)

27. The method of claim 1, wherein analyzing comprises using FISH.

28. The probe method of claim 1, wherein said probe is used as a biomarker for the early detection of early neoplastic events or cancer.

29. The method of claim 1, further comprising providing a 10q22 DNA gene probe and performing steps (c) and (d) with said 10q22 gene probe.

57. A method for predicting the progression or metastasis of non-small cell lung carcinoma and other carcinoma in a subject having said non-small cell lung carcinoma comprising:

(a) obtaining a test sample from a subject;
(b) providing an [RPL14, CD39L3, PMGM, or GC20] gene probe;
(c) contacting said probe with said test sample; and
(d) analyzing DNA from said test sample for loss of heterozygosity in RPL14,

wherein loss of RPL14 heterozygosity predicts progression or metastasis of said non-small cell lung carcinoma.

58. The method of claim 57, wherein said cancer is lung cancer further comprising providing a GC20 gene probe and performing steps (c) and (d) with said GC20 gene probe.

66. The method of claim 57, further comprising using providing a 10q22 DNA probe and performing steps (c) and (d) with said 10q22 gene probe.

69. A method of determining likelihood of predicting lung cancer relapse or development of a new primary lung cancer in a subject comprising determining genetic aberrations at chromosomal loci 3p21.3 or 10q22 in DNA loss of heterozygosity in the RPL14 gene in cells of bronchial tissue adjacent to tumor tissue from said subject, wherein abnormalities in DNA of loss of RPL14 heterozygosity in said adjacent tissue correlate with predicts lung cancer relapse or development of said lung cancer.

71. The method of claim 70, wherein said cancer is non-small cell lung carcinoma.

81. The method of claim 69, wherein an RPL 14, CD39L3, PMGM, or further comprising providing a GC20 gene probe and determining loss of heterozygosity in the GC20 gene in cells of bronchial tissue adjacent to tumor tissue from said subject.

84. The method of claim 82 69, further comprising use of providing a 10q22 DNA probe and determining loss of heterozygosity in the 10q22 region in cells of bronchial tissue adjacent to tumor tissue from said subject.

85. The method of claim 69, wherein said test sample comes from the same or contralateral lung.

86. The method of claim 69, wherein said test sample comes from nontumorous bronchial cells.

87. A method of identifying an individual to be segregated from a high risk lung cancer environment comprising:

(a) obtaining a test sample from a subject;
(b) providing an RPL14, CD39L3, PMGM, or GC20 gene probe
(c) contacting said probe with said test sample; and
(d) analyzing DNA from said test sample for loss of heterozygosity in RPL14,

whereby said analysis is used to identify loss of RPL14 heteroygosity identifies an individual who is highly susceptible to the development of lung cancer and who should not be exposed to a high risk environment.

88. The method of claim 87, further comprising providing a 10q22, GC20 or PTEN/MMAC1 gene probe and performing steps (c) and (d) with said 10q22, GC20 or PTEN/MMAC1 gene probe.